



1642

RAW SEQUENCE LISTING

DATE: 07/10/2002

PATENT APPLICATION: US/08/766,350B

TIME: 11:03:05

Input Set : A:\30414-20003.21.txt

Output Set: N:\CRF3\07102002\H766350B.raw

SEQUENCE LISTING

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JUL 16 2002

TECH CENTER 1600/2900

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Chatterjee, Malaya

7 Foon, Kenneth A.

8 Chatterjee, Sunil K.

10 (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY

11 11D10 AND METHODS OF USE THEREOF

13 (iii) NUMBER OF SEQUENCES: 58

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: MORRISON & FOERSTER

17 (B) STREET: 755 PAGE MILL ROAD

18 (C) CITY: PALO ALTO

19 (D) STATE: CA

20 (E) COUNTRY: USA

21 (F) ZIP: 94304-1018

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/08/766,350B

C--> 31 (B) FILING DATE: 13-Dec-1996

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Polizzi, Catherine M.

36 (B) REGISTRATION NUMBER: 40,130

37 (C) REFERENCE/DOCKET NUMBER: 30414-20003.21

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (415) 813-5600

41 (B) TELEFAX: (415) 494-0792

42 (C) TELEX: 706141

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 435 base pairs

49 (B) TYPE: nucleic acid

50 (C) STRANDEDNESS: single

51 (D) TOPOLOGY: linear

53 (ii) MOLECULE TYPE: DNA (genomic)

56 (ix) FEATURE:

57 (A) NAME/KEY: CDS

58 (B) LOCATION: 1..435

60 (ix) FEATURE:

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61      (A) NAME/KEY: mat_peptide
62      (B) LOCATION: 61
65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA      48
68 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro
69 -20      -15      -10      -5
71 GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT      96
72 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
73      1      5      10
75 GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC      144
76 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
77      15      20      25
79 ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT      192
80 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
81      30      35      40
83 AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA      240
84 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
85 45      50      55      60
87 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC      288
88 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
89      65      70      75
91 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT      336
92 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
93      80      85      90
95 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG      384
96 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
97      95      100      105
99 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT      432
100 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
101 110      115      120
103 GGG      435
104 Gly
105 125
108 (2) INFORMATION FOR SEQ ID NO: 2:
110      (i) SEQUENCE CHARACTERISTICS:
111          (A) LENGTH: 145 amino acids
112          (B) TYPE: amino acid
113          (D) TOPOLOGY: linear
115      (ii) MOLECULE TYPE: protein
117      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
119 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro
120 -20      -15      -10      -5
122 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
123      1      5      10
125 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
126      15      20      25
128 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
129      30      35      40
131 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys

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132 45          50          55          60
134 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
135          65          70          75
137 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
138          80          85          90
140 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
141          95          100          105
143 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
144          110          115          120
146 Gly
147 125
149 (2) INFORMATION FOR SEQ ID NO: 3:
151 (i) SEQUENCE CHARACTERISTICS:
152 (A) LENGTH: 461 base pairs
153 (B) TYPE: nucleic acid
154 (C) STRANDEDNESS: single
155 (D) TOPOLOGY: linear
157 (ii) MOLECULE TYPE: DNA (genomic)
160 (ix) FEATURE:
161 (A) NAME/KEY: CDS
162 (B) LOCATION: 1..459
164 (ix) FEATURE:
165 (A) NAME/KEY: mat_peptide
166 (B) LOCATION: 58
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
171 ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT      48
172 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
173 -19          -15          -10          -5
175 GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG      96
176 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
177          1          5          10
179 TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG      144
180 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
181          15          20          25
183 ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG      192
184 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
185          30          35          40          45
187 GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT      240
188 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
189          50          55          60
191 CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC      288
192 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
193          65          70          75
195 ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC      336
196 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
197          80          85          90
199 TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT      384
200 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
201          95          100          105

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203 CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC      432
204 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
205 110                               115                               120       125
207 GTC TAT CCA CTG GTC CCT GGA AGC TTG GG                                461
208 Val Tyr Pro Leu Val Pro Gly Ser Leu
209                               130
212 (2) INFORMATION FOR SEQ ID NO: 4:
214     (i) SEQUENCE CHARACTERISTICS:
215         (A) LENGTH: 153 amino acids
216         (B) TYPE: amino acid
217         (D) TOPOLOGY: linear
219     (ii) MOLECULE TYPE: protein
221     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
223 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
224 -19                               -15                               -10              -5
226 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
227                               1                               5                               10
229 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
230                               15                               20                               25
232 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
233 30                               35                               40              45
235 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
236                               50                               55              60
238 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
239                               65                               70              75
241 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
242                               80                               85              90
244 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
245 95                               100                              105
247 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
248 110                              115                              120              125
250 Val Tyr Pro Leu Val Pro Gly Ser Leu
251                               130
253 (2) INFORMATION FOR SEQ ID NO: 5:
255     (i) SEQUENCE CHARACTERISTICS:
256         (A) LENGTH: 321 base pairs
257         (B) TYPE: nucleic acid
258         (C) STRANDEDNESS: single
259         (D) TOPOLOGY: linear
265     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
267 GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT      60
269 CTCACCTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA      120
271 GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTGCCCCAAA      180
273 AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT      240
275 GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG      300
277 GGGACCAAGC TGGAAATAAA A                                     321
279 (2) INFORMATION FOR SEQ ID NO: 6:
281     (i) SEQUENCE CHARACTERISTICS:
282         (A) LENGTH: 321 base pairs

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283      (B) TYPE: nucleic acid
284      (C) STRANDEDNESS: single
285      (D) TOPOLOGY: linear
291      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
293 GANATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT      60
295 CTCACCTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA      120
297 GATGGAACCTT TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCTCCAAA      180
299 AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT      240
301 GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT GTCCGTACAC GTTCGGAGGG      300
303 GGGACCAAGC TGGAAATAAA A                                     321
305 (2) INFORMATION FOR SEQ ID NO: 7:
307      (i) SEQUENCE CHARACTERISTICS:
308          (A) LENGTH: 321 base pairs
309          (B) TYPE: nucleic acid
310          (C) STRANDEDNESS: single
311          (D) TOPOLOGY: linear
317      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
319 GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT      60
321 CTCACCTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA      120
323 GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCTCCAAA      180
325 AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT      240
327 GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA      300
329 GGCACCAAGC TGGAAATCAA A                                     321
331 (2) INFORMATION FOR SEQ ID NO: 8:
333      (i) SEQUENCE CHARACTERISTICS:
334          (A) LENGTH: 321 base pairs
335          (B) TYPE: nucleic acid
336          (C) STRANDEDNESS: single
337          (D) TOPOLOGY: linear
343      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
345 GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT      60
347 CTCACCTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA      120
349 GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCTCCAAA      180
351 AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT      240
353 GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA      300
355 GGCACCAAGC TGGAAATCAA A                                     321
357 (2) INFORMATION FOR SEQ ID NO: 9:
359      (i) SEQUENCE CHARACTERISTICS:
360          (A) LENGTH: 321 base pairs
361          (B) TYPE: nucleic acid
362          (C) STRANDEDNESS: single
363          (D) TOPOLOGY: linear
369      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
371 GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT      60
373 CTCACCTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA      120
375 GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCTCCAAA      180
377 AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT      240
379 GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA      300
381 GGCACCAAGC TGGAAATCAA A                                     321

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